



# **RAW SEQUENCE LISTING** **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

09/686,234A

Source:

1600

Date Processed by STIC:

7/18/02

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:**

**<http://www.uspto.gov/web/offices/pac/checker>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efb/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
Or  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002



**Does Not Comply** 1600  
**Corrected Diskette Needed**

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/686,234A

DATE: 07/18/2002  
TIME: 13:16:40

Input Set : A:\EP.txt  
Output Set: N:\CRF3\07182002\I686234A.raw

# SEQUENCE LISTING

2 (1) GENERAL INFORMATION:  
4 (i) APPLICANT: SOMMERVILLE, CHRIS  
5 SCHIEBLE, WOLF  
6 (ii) TITLE OF INVENTION: MODIFIED CELLULOSE SYNTHASE GENE  
7 FROM ARABIDOPSIS THALIANA CONFERS HERBICIDE RESISTANCE  
8 TO PLANTS  
10 (iii) NUMBER OF SEQUENCES: 2  
12 (iv) CORRESPONDENCE ADDRESS:  
13 (A) ADDRESSEE: PAUL A. GOTTLIEB, AGCTT  
14 DEPARTMENT OF ENERGY  
15 GC-62 (FORSTL) MS-6F-067  
16 (B) STREET: 1000 INDEPENDENCE AVE. S.W.  
17 (C) CITY: WASHINGTON, D.C.  
C--> 18 (F) ZIP: 20585  
20 (v) COMPUTER READABLE FORM:  
21 (A) MEDIUM TYPE: FLOPPY DISK  
22 (B) COMPUTER: IBM PC COMPATIBLE  
23 (C) OPERATING SYSTEM: MS-DOS  
24 (D) SOFTWARE: WORDPERFECT 8  
26 (vi) CURRENT APPLICATION DATA:  
C--> 27 (A) APPLICATION NUMBER: US/09/686,234A  
C--> 28 (B) FILING DATE: 11-Oct-2000  
31 (viii) ATTORNEY/AGENT INFORMATION:  
32 (A) NAME: SMITH, BRADLEY  
33 (B) REGISTRATION NUMBER: 334436  
34 (C) REFERENCE/DOCKET NUMBER: S-93994  
C--> 36 (ix) TELECOMMUNICATION INFORMATION:  
37 (A) TELEPHONE: 630-252-2160  
38 (B) TELEFAX: 630-252-2779

The type of errors shown exist throughout  
the Sequence Listing. Please check subsequent  
sequences for similar errors.

## ERRORED SEQUENCES

43 (2) INFORMATION FOR SEQ ID NO: 1:  
45 (i) SEQUENCE CHARACTERISTICS:  
46 (A) LENGTH: 3563 NUCLEOTIDES  
47 (B) TYPE: NUCLEIC ACID  
48 (C) STRANDEDNESS: DOUBLE STRANDED  
49 (D) TOPOLOGY: LINEAR  
C--> 52 (ii) MOLECULE TYPE: cDNA  
58 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
E--> 60 ① atcccaagat tctctcttc gtcttcctta taaactatct ctctgtagag aagaagctt

↑  
Nucleotide numbers  
must be on the right margin;  
and must be a maximum  
number of 60  
per line  
per  
Sect. 1.823(a)

*must be on right - max. of 1000*

## RAW SEQUENCE LISTING

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Input Set : A:\EP.txt

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E--> 61      61 ggatccagat tgagagagat tcagagagcc acatcaccac actccatctt cagatctcat
E--> 62      121 gatttgaact attccgacgt ttcggtgttg gaagcaacta agtgacaaat ggaatccgaa
E--> 63      181 ggggaaaccg cgggaaagcc gatgaagaac attgttccgc agacttgcca gatctgtagt
E--> 64      241 gacaatgttg gcaagactgt tgatggagat cgttttgttg cttgtgatat ttgttcattc
E--> 65      301 ccagtttgtc ggccttgcta cgagtatgag aggaaagatg ggaatcaatc ttgtcctcag
E--> 66      361 tgcaaaacca gatacaagag gctcaaaggt agtccctgcta ttccctggtg taaagacgag
E--> 67      421 gatggcttag ctgatgaagg tactgttgag ttcaactacc ctcagaagga gaaaatttca
E--> 68      481 gageggatgc ttggttgcca tcttactcgt gggaaggagg aggaaatggg ggaaccccag
E--> 69      541 tatgataaag aggtctctca caatcatctt cctcgtctca cgagcagaca agatacttca
E--> 70      601 ggagagtttt ctgctgcctc acctgaacgc ctctctgtat cttctactat cgtctgggga
E--> 71      661 aagcgcttcc cctattcatc agatgtcaat caatcaccaa atagaaggat tgtggatcct
E--> 72      721 gttggactcg ggaatgtagc ttggaaggag agagttgatg gctggaaaat gaagcaagag
E--> 73      781 aagaatactg gtcctgtcag cagcgaggct gcttctgaaa gaggtggagt agatattgat
E--> 74      841 gccagcacag atatcctagc agatgaggct ctgctgaatg acgaagcgag gcagcctctg
E--> 75      901 tcaaggaaag tttcaattcc ttcacacagg atcaatcctt acagaatggt tattatgctg
E--> 76      961 cggettgtta tcctttgtct cttcttgcac taccgtataa caaacccagt gccaaatgcc
E--> 77      1021 tttgctctat ggctggtctc tgtgatagt gagatctggt ttgccttacc ctggattttg
E--> 78      1081 gatcagtttc ccaagtgggt tcctgtgaac cgtgaaacct acctcgacag gcttgcctta
E--> 79      1141 agatatgacg gtgaagggtga gccatcacag ttagctgctg ttgacatttt cgtgagtact
E--> 80      1201 gttgaccctc tgaaggagcc accccttggt acagccaaca cagtgccttc tattctggct
E--> 81      1261 gttgactacc cagttgacaa ggtgtcctgt tatgtttttg atgatgggtg tgcattgcta
E--> 82      1321 tcatttgaat cacttgacga aacatcacag tttgtcctga aatgggtacc attttgcaag
E--> 83      1381 aatatatgca tagagcctcg tgcaccagaa tggtagcttg ctgcgaaaat agattacttg
E--> 84      1441 aaggataaag ttcagacatc atttgtcaaa gatcgtagag ctatgaagag ggaatatgag
E--> 85      1501 gaatttataa tccgaatcaa tgcacttggt tccaaagccc taaaatgtcc tgaagaaggg
E--> 86      1561 tgggttatgc aagatggcac accgtggcct ggaaataata caggggacca tccaggaatg
E--> 87      1621 atccaggtct tcttagggca aaatgggtgga cttgatgcag agggcaatga gctcccgcgt
E--> 88      1681 ttggtatatg tttctcgaga aaagcgacca ggattccagc accacaaaaa ggctgggtgct
E--> 89      1741 atgaatgcac tggtagagat ttcagcagtt cttaccaatg gacctttcat cttgaatctt
E--> 90      1801 gatttgtgac attacataaa taacagcaaa gccttaagag aagcaatgtg cttcctgatg
E--> 91      1861 gacccaaacc tcgggaagca agtttgttat gttcagttcc cacaagattt tgatgggtatc
E--> 92      1921 gataagaacg atagatatgc taatcgtaat accgtgttct ttgatattaa cttgagaggt
E--> 93      1981 ttagatggga ttcaaggacc tgtatatgtc ggaactggat gtgttttcaa cagaacagca
E--> 94      2041 ttatacggtt atgaacctcc aataaaagta aaacacaaga agccaagtct tttatctaag
E--> 95      2101 ctctgtgggt gatcaagaaa gaagaattcc aaagctaaga aagagtcgga caaaaagaaa
E--> 96      2161 tcaggcaggc atactgactc aactgttccct gtattcaacc tcgatgacat agaagaggga
E--> 97      2221 gttgaagggt ctggttttga tgatgaaaag gcgctcttaa tgcgcaaat gagcctggag
E--> 98      2281 aagcgatttg gacagctgac tgtttttgtt gcttctacc taatggaaaa tgggtggtgtt
E--> 99      2341 cctccttcag caactccaga aaacctctc aaagaggcta tccatgtcat tagttgtggt
E--> 100     2401 tatgaggata agtcagattg gggaaatggag attggatgga tctatggttc tgtgacagaa
E--> 101     2461 gatattctga ctgggttcaa aatgcatgcc cgtggatggc gatccattta ctgcatgcct
E--> 102     2521 aagcttccag ctttcaaggg ttctgtcctt atcaatcttt cagatcgtct gaaccaagtg
E--> 103     2581 ctgaggtggg ctttaggttc agttgagatt ctcttcagtc ggcattgtcc tatatggtat
E--> 104     2641 gggtacaatg ggaggctaaa atttcttgag aggtttgcgt atgtgaacac caccatctac
E--> 105     2701 cctatcacct ccattcctct tctcatgtat tgtacattgc tagccgtttg tctcttcacc
E--> 106     2761 aaccagttta ttattcctca gattagtaac attgcaagta tatggtttct gtctctcttt
E--> 107     2821 ctctccattt tcgccacggg tatactagaa atgaggtgga gtggcgtagg catagacgaa
E--> 108     2881 tgggtggagaa acgagcagtt ttgggtcatt ggtggagtat ccgctcattt attcgtctgtg
E--> 109     2941 tttcaaggta tcctcaaagt ccttgccggt attgacacaa acttcacagt tatctcaaaa

```

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TIME: 13:16:40

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*Some error*

```

E--> 110 3001 gcttcagatg aagacggaga ctttgctgag ctctacttgt tcaaatggac aacacttctg
E--> 111 3061 attccgccaa cgacgtgct cattgtaaac ttagtgggag ttgttgcagg agtctcttat
E--> 112 3121 gctatcaaca gtggatacca atcatgggga ccactctttg gtaagttggt ctttgccttc
E--> 113 3181 tgggtgattg ttcacttgta ccctttcctc aagggttga tgggtcgaca gaaccggact
E--> 114 3241 cctaccattg ttgtggtctg gtctgttctc ttggcttcta tcttctcggt gttgtgggtt
E--> 115 3301 aggattgac ccttcactag ccgagtcact ggcccggaca ttctggaatg tggaatcaac
E--> 116 3361 tgttgagaag cgagcaaata tttacctgtt ttgagggtta aaaaaaacac agaatttaaa
E--> 117 3421 ttatttttca ttgttttatt tgttcacttt tttacttttg ttgtgtgtat ctgtctgttc
E--> 118 3481 gttcttctgt cttggtgtca taaatttatg tgtagaatat atcttactct agttactttg
E--> 119 3541 gaaagttata attaaagtga aag

```

124 (2) INFORMATION FOR SEQ ID NO: 2:

126 (i) SEQUENCE CHARACTERISTICS:

127 (A) LENGTH: 3563 NUCLEOTIDES

128 (B) TYPE: NUCLEIC ACID

129 (C) STRANDEDNESS: DOUBLE STRANDED

130 (D) TOPOLOGY: LINEAR

132 (ii) MOLECULE TYPE: cDNA

134 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

*Some error*

```

E--> 136 1 atcccaagat tctcctcttc gtcttcctta taaactatct ctctgtagag aagaaagctt
E--> 137 61 ggatccagat tgagagagat tcagagagcc acatcaccac actccatctt cagatctcat
E--> 138 121 gatttgaact attccgacgt ttcggtggtg gaagcaacta agtgacaaat ggaatccgaa
E--> 139 181 ggggaaaccg cgggaaagcc gatgaagaac attgttccgc agacttgcca gatctgtagt
E--> 140 241 gacaatgttg gcaagactgt tgatggagat cgttttgggt cttgtgatat ttgttcattc
E--> 141 301 ccagtttgtc ggccttgcta cgagtatgag aggaaagatg ggaatcaatc ttgtcctcag
E--> 142 361 tgcaaaacca gatacaagag gctcaaaggt agtcctgcta ttcttggtga taaagacgag
E--> 143 421 gatggcttag ctgatgaagg tactgttgag ttcaactacc ctcaagaagg gaaaatttca
E--> 144 481 gageggatgc ttggttgga tcttactcgt gggaaggagg aggaaatggg ggaacccag
E--> 145 541 tatgataaag aggtctctca caatcatctt cctcgtctca cgagcagaca agatacttca
E--> 146 601 ggagagtttt ctgtgcctc acctgaacgc ctctctgtat cttctactat cgctggggga
E--> 147 661 aagcgcttc cctattcatc agatgtcaat caatcaccaa atagaaggat tgtggatcct
E--> 148 721 gttggactcg ggaatgtagc ttggaaggag agagttgatg gctggaaaat gaagcaagag
E--> 149 781 aagaatactg gtctgtcag cacgcaggct gcttctgaaa gaggtggagt agatattgat
E--> 150 841 gccagcacag atatcctagc agatgaggct ctgctgaatg acgaagcgag gcagcctctg
E--> 151 901 tcaaggaaaag tttcaattcc ttcatacagg atcaatcctt acagaatggt tattatgctg
E--> 152 961 cggcttggtta tcctttgtct cttcttgcat taccgtataa caaacccagt gccaatgcc
E--> 153 1021 tttgctctat ggctggtctc tgtgatagt gagatctggt ttgccttate ctggattttg
E--> 154 1081 gatcagtttc ccaagtgggt tcctgtgaac cgtgaaacct acctcgacag gcttgcttta
E--> 155 1141 agatatgate gtgaagggtga gccatcacag ttagctgctg ttgacatttt cgtgagtact
E--> 156 1201 gttgacctc tgaaggagcc accccttggt acagccaaca cagtgcctc tattctggct
E--> 157 1261 gttgactacc cagttgacaa ggtgtcctgt tatgtttttg atgatgggtc tgctatgtta
E--> 158 1321 tcatttgaat cacttgacga aacatcacag tttgctcgta aatgggtacc attttgcaag
E--> 159 1381 aaatatagca tagagcctcg tgcaccagaa tggtaacttg ctgcgaaaat agattacttg
E--> 160 1441 aaggataaag ttcagacatc atttgtcaaa gatcgtagag ctatgaagag ggaatatgag
E--> 161 1501 gaatttaaaa tccgaatcaa tgcacttggt tccaaagccc taaaatgtcc tgaagaaggg
E--> 162 1561 tgggttatgc aagatggcac accgtggcct ggaaataata caggggacca tccaggaatg
E--> 163 1621 atccaggtct tcttagggca aaatggtgga cttgatgcag agggcaatga gctcccgcgt
E--> 164 1681 ttggtatatg tttctcgaga aaagcgacca ggattccagc accacaaaaa ggctgggtgct
E--> 165 1741 atgaatgcac tgggtgagagt ttcagcagtt cttaccaatg gacctttcat cttgaatctt
E--> 166 1801 gattgtgatc attacataaa taacagcaaa gccttaagag aagcaatgtg cttcctgatg

```

## RAW SEQUENCE LISTING

DATE: 07/18/2002

PATENT APPLICATION: US/09/686,234A

TIME: 13:16:40

Input Set : A:\EP.txt

Output Set: N:\CRF3\07182002\I686234A.raw

*Summary*

```

E--> 167 1861 gacccaaacc tcgggaagca agtttggttat gttcagttcc caciaagatt tgatggtatc
E--> 168 1921 gataagaacg atagatatgc taatcgtaat accgtgttct ttgatattaa cttgagaggt
E--> 169 1981 ttagatggga ttcaaggacc tgtatatgtc ggaactggat gtgttttcaa cagaacagca
E--> 170 2041 ttatacgggt atgaacctcc aataaaaagta aaacacaaga agccaagtct tttatctaag
E--> 171 2101 ctctgtggtg gatcaagaaa gaagaattcc aaagctaaga aagagtcgga caaaaagaaa
E--> 172 2161 tcaggcaggc atactgactc aactgttcct gtattcaacc tcgatgacat agaagagggg
E--> 173 2221 gttgaagggt ctggttttga tgatgaaaag gcgctcttaa tgcgcgaaat gaggctggag
E--> 174 2281 aagcgatttg gacagtctgc tgtttttgtt gcttctaccc taatggaaaa tgggtggtgtt
E--> 175 2341 cctccttcag caactccaga aaacctcttc aaagaggcta tccatgtcat tagttgtggt
E--> 176 2401 tatgaggata agtcagattg gggaaatggag attggatgga tctatgggtc tgtgacagaa
E--> 177 2461 gatattctga ctgggttcaa aatgcatgcc cgtggatggc gatccattta ctgcatgcct
E--> 178 2521 aagcttcag ctttcaaggg ttctgtcct atcaatcttt cagatcgtct gaaccaagtg
E--> 179 2581 ctgaggtggg ctttaggttc agttgagatt ctcttcagtc ggcattgtcc tatatggtat
E--> 180 2641 gggtacaatg ggaggctaaa atttcttgag aggtttgcgt atgtgaacac caccatctac
E--> 181 2701 cctatcacct ccattcctct tctcatgtat tgtacattgc tagccgtttg tctcttcacc
E--> 182 2761 aaccagttta ttattcctca gattagtaac attgcaagta tatggtttct gtctctcttt
E--> 185 2821 ctctccattt tcgccacggg tatactagaa atgaggtgga gtggcgtagg catagacgaa
E--> 186 2881 tgggtggagaa acgagcagtt ttgggtcatt ggtggagtat ccgctcattt attcgtctgtg
E--> 187 2941 tttcaaggta tctcaaagt ccttgccggg attgacacaa acttcacagt tacctcaaaa
E--> 188 3001 gcttcagatg aagacggaga ctttgctgag ctctacttgt tcaaattggac aacacttctg
E--> 189 3061 attccgccaa cgacgtgct cattgtaaac ttagtgggag ttgttgagg agtctcttat
E--> 190 3121 gctatcaaca gtggatacca atcatgggga ccactctttg ataagttgtt ctttgcttc
E--> 191 3181 tgggtgattg ttcacttgta cccttctc aagggtttga tgggtcgaca gaaccggact
E--> 192 3241 cctaccattg ttgtggtctg gtctgttctc ttggcttcta tcttctcgtt gttgtgggtt
E--> 193 3301 aggattgac ccttactag ccgagtcact ggcccggaca ttctggaatg tggaaatcaac
E--> 194 3361 tgttgagaag cgagcaaata tttacctgtt ttgaggggta aaaaaaacac agaatttaaa
E--> 195 3421 ttatttttca ttgttttatt tgttcacttt tttacttttg ttgtgtgtat ctgtctgttc
E--> 196 3481 gttcttctgt cttggtgtca taaatttatg tgtagaatat atcttactct agttactttg
E--> 197 3541 gaaagttata attaaagtga aag

```

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/686,234A

DATE: 07/18/2002

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Input Set : A:\EP.txt

Output Set: N:\CRF3\07182002\I686234A.raw

L:18 M:220 C: Keyword misspelled or invalid format, [(F) ZIP:]  
L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:36 M:220 C: Keyword misspelled or invalid format, [(ix) TELECOMMUNICATION INFORMATION:]  
L:52 M:220 C: Keyword misspelled or invalid format, [(ii) MOLECULE TYPE:]  
L:60 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7  
L:60 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:61 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0  
L:61 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7  
L:61 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:62 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0  
L:62 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7  
L:62 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:63 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0  
L:63 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7  
L:63 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:64 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0  
L:64 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7  
L:64 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:65 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0  
L:65 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7  
L:65 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:66 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0  
L:66 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7  
L:66 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:67 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0  
L:67 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7  
L:67 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:68 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0  
L:68 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7  
L:68 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:69 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0  
L:69 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7  
L:69 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:70 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0  
L:70 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7  
L:70 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:71 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0  
L:71 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7  
L:71 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:72 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0  
L:72 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7  
L:72 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:73 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0  
L:73 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7  
L:73 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:74 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0  
L:74 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7

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Output Set: N:\CRF3\07182002\I686234A.raw

L:74 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:75 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0  
L:75 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7  
L:75 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:76 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0  
L:76 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7  
L:76 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:77 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0  
L:77 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7  
L:77 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:78 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0  
L:78 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7  
L:78 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:79 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0  
L:79 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7  
L:79 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:80 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0  
L:80 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7  
L:80 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:81 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0  
L:81 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7  
L:81 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:82 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0  
L:82 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7  
L:82 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:83 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0  
L:83 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7  
L:83 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:84 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0  
L:84 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7  
L:84 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:85 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0  
L:85 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7  
L:85 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:86 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0  
L:86 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7  
L:86 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:87 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0  
L:87 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7  
L:87 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:88 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0  
L:88 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7  
L:88 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:89 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0  
L:89 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7  
L:89 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:90 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0  
L:90 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7  
L:90 M:333 E: Wrong sequence grouping, Amino acids not in groups!



## VERIFICATION SUMMARY

DATE: 07/18/2002

PATENT APPLICATION: US/09/686,234A

TIME: 13:16:41

Input Set : A:\EP.txt

Output Set: N:\CRF3\07182002\I686234A.raw

L:91 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0  
L:91 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7  
L:91 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:92 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0  
L:92 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7  
L:92 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:93 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0  
L:93 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7  
L:93 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:94 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0  
L:94 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7  
L:94 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:95 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0  
L:95 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7  
L:95 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:96 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0  
L:96 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7  
L:96 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:97 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0  
L:97 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7  
L:97 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:98 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0  
L:98 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7  
L:98 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:99 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0  
L:99 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7  
L:99 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:100 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0  
L:100 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7  
L:100 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:101 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0  
L:101 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7  
L:101 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:102 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0  
L:102 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7  
L:102 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:103 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0  
L:103 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7  
L:103 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:104 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0  
L:104 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7  
L:104 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:105 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0  
L:105 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7  
L:105 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:106 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0  
L:106 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7  
L:106 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:107 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0



## VERIFICATION SUMMARY

DATE: 07/18/2002

PATENT APPLICATION: US/09/686,234A

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Input Set : A:\EP.txt

Output Set: N:\CRF3\07182002\I686234A.raw

L:107 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7  
L:107 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:108 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0  
L:108 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7  
L:108 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:109 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0  
L:109 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7  
L:109 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:110 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0  
L:119 M:204 E: No. of Bases differ, LENGTH:Input:3563 Counted:0 SEQ:1  
L:197 M:204 E: No. of Bases differ, LENGTH:Input:3563 Counted:0 SEQ:2